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<!--StartFragment-->RESULT 6
AGLA_RHIME
ID   AGLA_RHIME                      Reviewed;          551 AA.
AC   Q9Z3R8;
DT   30-MAY-2000, integrated into UniProtKB/Swiss-Prot.
DT   02-NOV-2001, sequence version 2.
DT   24-JUL-2007, entry version 44.
DE   Probable alpha-glucosidase (EC 3.2.1.20).
GN   Name=agla; OrderedLocusNames=R00698; ORFNames=SMc03064;
OS   Rhizobium meliloti (Sinorhizobium meliloti).
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX   NCBI_TaxID=382;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX   MEDLINE=99328961; PubMed=10400573;
RA   Willis L.B., Walker G.C.;
RT   "A novel Sinorhizobium meliloti operon encodes an alpha-glucosidase
RT   and a periplasmic-binding-protein-dependent transport system for
RT   alpha-glucosides.";
RL   J. Bacteriol. 181:4176-4184(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=1021;
RX   MEDLINE=21396507; PubMed=11481430; DOI=10.1073/pnas.161294398;
RA   Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA   Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA   Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA   Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
RA   Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
RT   "Analysis of the chromosome sequence of the legume symbiont
RT   Sinorhizobium meliloti strain 1021.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
CC   -!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing 1,4-
CC   linked alpha-D-glucose residues with release of alpha-D-glucose.
CC   -!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
CC   -----
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----
DR   EMBL; AF045609; AAD12047.1; -; Genomic_DNA.
DR   EMBL; AL591784; CAC45270.1; -; Genomic_DNA.
DR   HSSP; P21332; 1UOK.
DR   GenomeReviews; AL591688_GR; R00698.
DR   KEGG; sme:SMc03064; -.
DR   BioCyc; SMEL266834:SMC03064-MONOMER; -.
DR   GO; GO:0004558; F:alpha-glucosidase activity; IEA:EC.
DR   InterPro; IPR006047; Glyco_hydro_13_cat.
DR   InterPro; IPR006589; Glyco_hydro_13_sub_cat.
DR   InterPro; IPR013781; Glyco_hydro_cat.
DR   Gene3D; G3DSA:3.20.20.80; Glyco_hydro_cat; 1.
DR   Pfam; PF00128; Alpha-amylase; 1.
DR   SMART; SM00642; Aamy; 1.
PE   3: Inferred from homology;
KW   Complete proteome; Glycosidase; Hydrolase.
FT   CHAIN           1           551      Probable alpha-glucosidase.
FT                                     /FTid=PRO_0000054312.
FT   ACT_SITE       212       212      Nucleophile (By similarity).
FT   ACT_SITE       272       272      Proton donor (By similarity).
FT   ACT_SITE       345       345      By similarity.
FT   CONFLICT       13        13        P -> A (in Ref. 1).

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FT	CONFLICT	20	21	GA -> RP (in Ref. 1).
FT	CONFLICT	402	415	YGIQFWPDFKGRDG -> MASSSGPTSSAGR (in Ref. 1).
FT				
FT	CONFLICT	445	460	PRAVAVQEGDPASVLH -> RGRCRAGGRPGLGAA (in Ref. 1).
FT				
SQ	SEQUENCE	551 AA;	62576 MW;	BB7BD3E17C935509 CRC64;

Query Match 54.5%; Score 1595.5; DB 1; Length 551;
 Best Local Similarity 57.3%; Pred. No. 9.7e-113;
 Matches 294; Conservative 74; Mismatches 130; Indels 15; Gaps 6;

Qy	3	EWNRGAVTYQVYPRSFQDSNGDGIGDLPGITARLEYLADLGVDAVWLSPPFFKSPMKDMGY	62
		: : : : : : : : : : : :	
Db	16	DWNRGAVIYQYPRSFQDNTNGDGIGDLQGITARLPHIAGLGADAIWISPFFTSPMRDFGY	75
Qy	63	DVSDYCDVDPVFGTILADFDALLARAHELGLKVIIDQVLSHSDLHPAFVTSRSDRVNPKA	122
		: : : : : : : : : : : : : : : :	
Db	76	DVSNYVDVDPFIFGTLEDFDALIAEAHRLGLRVMDLVLSHTSDRHPWFVESRSSRSNKA	135
Qy	123	DWYVWADPKPDGSPNNWLSVFGGSAAWADARRKQYYLHNFLT SQPDLNHNPKVQDWAL	182
		: : : : : : : : : : : :	
Db	136	DWYVWADSKPDGTPPNNWLSIFGGSAAQWDPTRLQYYLHNFLT SQPDLNHNPKVQDEALL	195
Qy	183	DNMRFLDRGVDGFRFDTVNYFFHDPLLRSNPA---DHRNKPEADG-NPYGMQYHLHDKN	238
		: : : : : : : : : : : : : : : : :	
Db	196	AVERFWLERGVDGFRDITINFYFHDRELDRNPALVPERRNASTAPAVNPNYQEHYDKN	255
Qy	239	QPENLIWMERIVLLDQYGA-ASVGEMGESHHAIRMMGDYTAGP-RLHQCYSEFFMGYE-	295
		: : : : : : : : : : : : : : : : : : : :	
Db	256	RPENLEFLKRFRAVMDEFFPAIAAVGEVGSQGRLEIAGEYTSGGDKVHMCYAFEFLLAPDR	315
Qy	296	YTANLFRDRIESFFKGAPKGNPMWAFSNHDVVRHVSRAWKHGLTPEAVAKQTGALLLSLE	355
		: : : : : : : : : : : :	
Db	316	LTPQRVAEVLDRDFHRAAPEGWACWAFSNHDVVRHVSRAWGVTDHDAHAKLLASLLMSLR	375
Qy	356	GSICLWEGEELGQTDTELALDELDPQGIVFWPEPIGRDNTRTPMVWDA SPHGGSFTVTP	415
		: : : : : : : : : : : : : : : : : : : :	
Db	376	GTVCYIQGEELALAEALDYEDLQDPYGIQFWPDFKGRDGRCTPMVWESLPDGGFSATP	435
Qy	416	WLPVKPEQAARHVAGQTGDAASVLESYRAMLAFFRAEPALRTGRTRFLDLAEPVLGEVRG	475
		: : : : : : : : : : : : : : : : : :	
Db	436	WLPISQSHIPRAVAVQEGDPASVLHHYRRFLAFRKANPALARGEIEFVETRGSLLGLFLRS	495
Qy	476	EGEGAILCLFNLS-----PVARGVAVEGVG	500
		: : : : : : : : : :	
Db	496	HGNEKVFCLFNMSDEAATKELPMKRLPLEGHG	528

<!--EndFragment-->